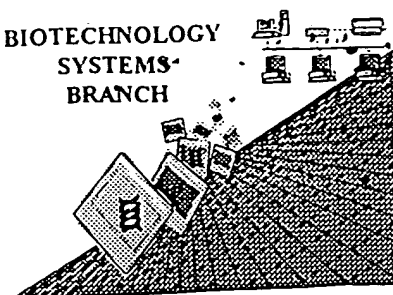


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/761534  
Source: DIPE  
Date Processed by STIC: 10/11/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

## RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/761,534

TIME: 13:34:44

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

4 <110> APPLICANT: Huang, Qian  
 5 Richmond, Joan F.L.  
 6 Cho, Bryan K.  
 7 Palliser, Deborah  
 8 Chen, Jianzhu  
 9 Eisen, Herman N.  
 10 Young, Richard A.  
 12 <120> TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
 13 Protein Fusion Proteins Maps To A Discrete Domain and is  
 14 CD4+T Cell-Independent  
 17 <130> FILE REFERENCE: 0399.2006-003  
 19 <140> CURRENT APPLICATION NUMBER: US 09/761,534  
 20 <141> CURRENT FILING DATE: 2001-01-16  
 22 <150> PRIOR APPLICATION NUMBER: PCT/US00/32831  
 23 <151> PRIOR FILING DATE: 2000-12-01  
 25 <150> PRIOR APPLICATION NUMBER: US 60/176,143  
 26 <151> PRIOR FILING DATE: 2000-01-14  
 28 <160> NUMBER OF SEQ ID NOS: 25  
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0 ✓  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 8  
 34 <212> TYPE: PRT  
 35 <213> ORGANISM: Unknown  
 37 <220> FEATURE:  
 38 <223> OTHER INFORMATION: Peptide Liberated From P1 ✓  
 40 <400> SEQUENCE: 1  
 41 Ser Ile Tyr Arg Tyr Tyr Gly Leu  
 42 1 5  
 45 <210> SEQ ID NO: 2  
 46 <211> LENGTH: 8  
 47 <212> TYPE: PRT  
 48 <213> ORGANISM: Unknown ✓  
 50 <220> FEATURE:  
 51 <223> OTHER INFORMATION: Ova Peptide ✓  
 53 <400> SEQUENCE: 2  
 54 Ser Ile Ile Asn Phe Glu Lys Leu  
 55 1 5  
 58 <210> SEQ ID NO: 3  
 59 <211> LENGTH: 8  
 60 <212> TYPE: PRT ✓  
 61 <213> ORGANISM: Unknown  
 63 <220> FEATURE:  
 64 <223> OTHER INFORMATION: Alpha KG Peptide ✓  
 66 <400> SEQUENCE: 3  
 67 Leu Ser Pro Phe Pro Phe Asp Leu  
 68 1 5  
 71 <210> SEQ ID NO: 4

Does Not Comply  
Corrected Diskette Needed

Does Not Comply  
Corrected Diskette Needed

220 and 223 } Artificial Sequences  
 check diskette

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/761,534

DATE: 10/11/2001

TIME: 13:34:44

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

```

72 <211> LENGTH: 5
73 <212> TYPE: PRT
74 <213> ORGANISM: Unknown
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Octapeptide ✓
79 <400> SEQUENCE: 4
80 Ser Tyr Arg Gly Leu
81 1 5
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 1260
86 <212> TYPE: DNA
87 <213> ORGANISM: Mycobacterium Tuberculosis hsp70 cDNA ✓
89 <220> FEATURE:
90 <221> NAME/KEY: CDS
W--> 91 <222> LOCATION: (0)...(1260)
93 <400> SEQUENCE: 5
94 atg gct cgt gcg gtc ggg atc gac ctc ggg acc acc aac tcc gtc gtc 48
95 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
96 1 5 10 15
98 tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc gag ggc 96
99 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
100 20 25 30
102 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
103 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
104 35 40 45
106 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
107 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
108 50 55 60
110 acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc ata gag 240
111 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
112 65 70 75 80
114 att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc att ctg 288
115 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
116 85 90 95
118 atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac att acc 336
119 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
120 100 105 110
122 gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag cgt cag 384
123 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
124 115 120 125
126 gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtg ctg cgg atc 432
127 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
128 130 135 140
130 gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctc gac aag ggc 480
131 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
132 145 150 155 160
134 gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc act ttc 528
135 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
136 165 170 175

```

## RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/761,534

TIME: 13:34:44

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

```

138 gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc 576
139 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
140 180 185 190
142 act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc 624
143 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
144 195 200 205
146 gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atg gat ctg 672
147 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
148 210 215 220
150 acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag 720
151 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
152 225 230 235 240
154 gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc 768
155 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
156 245 250 255
158 tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag 816
159 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
160 260 265 270
162 ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc 864
163 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
164 275 280 285
166 act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att tcg gtg 912
167 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
168 290 295 300
170 tcg gag atc gat cac gtt gtg ctc gtg ggt ggt tcg acc cgg atg ccc 960
171 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
172 305 310 315 320
174 gcg gtg acc gat ctg gtc aag gaa ctc acc ggc ggc aag gaa ccc aac 1008
175 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
176 325 330 335
178 aag ggc gtc aac ccc gat gag gtt gtc gcg gtg gga gcc gct ctg cag 1056
179 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
180 340 345 350
182 gcc ggc gtc ctc aag ggc gag gtg aaa gac gtt ctg ctg ctt gat gtt 1104
183 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Asp Val
184 355 360 365
186 acc ccg ctg agc ctg ggt atc gag acc aag ggc ggg gtg atg acc agg 1152
187 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
188 370 375 380
190 ctc atc gag cgc aac acc acg atc ccc acc aag cgg tcg gag act ttc 1200
191 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
192 385 390 395 400
194 acc acc gcc gac gac aac caa ccg tcg gtg cag atc cag gtc tat cag 1248
195 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
196 405 410 415
198 ggg gag cgt gag 1260
199 Gly Glu Arg Glu
200 420
203 <210> SEQ ID NO: 6

```

## RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/761,534

TIME: 13:34:44

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

204 &lt;211&gt; LENGTH: 420

205 &lt;212&gt; TYPE: PRT

206 &lt;213&gt; ORGANISM: Mycobacterium Tuberculosis hsp70 cDNA

208 &lt;400&gt; SEQUENCE: 6

```

209 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
210 1      5      10      15
211 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
212      20      25      30
213 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
214      35      40      45
215 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
216      50      55      60
217 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
218 65      70      75      80
219 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
220      85      90      95
221 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
222      100     105     110
223 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
224      115     120     125
225 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
226      130     135     140
227 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
228 145     150     155     160
229 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
230      165     170     175
231 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
232      180     185     190
233 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
234      195     200     205
235 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
236      210     215     220
237 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
238 225     230     235     240
239 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
240      245     250     255
241 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
242      260     265     270
243 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
244      275     280     285
245 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
246      290     295     300
247 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
248 305     310     315     320
249 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
250      325     330     335
251 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
252      340     345     350
253 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val

```

## RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/761,534

TIME: 13:34:44

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

```

254          355          360          365
255 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
256          370          375          380
257 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
258 385          390          395          400
259 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
260          405          410          415
261 Gly Glu Arg Glu
262          420
265 <210> SEQ ID NO: 7
266 <211> LENGTH: 630
267 <212> TYPE: DNA
268 <213> ORGANISM: Unknown
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Segment II of TBhsp70 ok
273 <221> NAME/KEY: CDS
W--> 274 <222> LOCATION: (0)...(631)
275 <223> OTHER INFORMATION: Segment II of TBhsp70 ok
277 <400> SEQUENCE: 7
278 gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc act ttc 48
279 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
280 1          5          10          15
282 gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc 96
283 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
284          20          25          30
286 act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc 144
287 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
288          35          40          45
290 gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atg gat ctg 192
291 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
292          50          55          60
294 acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag 240
295 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
296 65          70          75          80
298 gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc 288
299 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
300          85          90          95
302 tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag 336
303 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
304          100          105          110
306 ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc 384
307 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
308          115          120          125
310 act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att tcg gtg 432
311 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
312          130          135          140
314 tcg gag atc gat cac gtt gtg ctc gtg ggt ggt tcg acc cgg atg ccc 480
315 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
316 145          150          155          160

```

<210> SEQ ID NO 16  
<211> LENGTH: 36  
<212> TYPE: DNA  
<213> ORGANISM: ~~Unknown~~  
<220> FEATURE:  
<223> OTHER INFORMATION:  
<400> SEQUENCE: 16  
ggaattccta tctagtcact tgccctcccg gccgtc

Entered

36

actual file contents

as of 11/05/01

2:03 pm

A 213 response of "unknown" requires  
an explanation in field 223. mva

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/761,534

DATE: 10/11/2001

TIME: 13:34:45

Input Set : A:\0399.2006-003SEQLIST.txt

Output Set: N:\CRF3\10112001\I761534.raw

L:91 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...  
(1260)  
L:274 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (0)...  
(631)  
L:383 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION: (0)...  
(1929)  
L:654 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: (0)...  
(627)  
L:793 M:258 W: Mandatory Feature missing, (<220>) FEATURE:  
L:793 M:258 W: Mandatory Feature missing, (<223>) OTHER INFORMATION:

*Errors*